

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/527,370  
Source: PCR  
Date Processed by STIC: 3/3/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/527,370

TIME: 12:59:01

Input Set : A:\18965-002US1.TXT

Output Set: N:\CRF4\03032006\J527370.raw

```

4 <110> APPLICANT: Sogabe, Atsushi
5      Oka, Masanori
6      Inagaki, Kenji
7      Hatta, Takashi
8      Nishise, Hiroshi
10 <120> TITLE OF INVENTION: NOVEL GLYCEROL KINASE, GENE THEREOF AND
11      METHOD FOR PRODUCING THE GLYCEROL KINASE USING THE GENE
13 <130> FILE REFERENCE: 18965-002US1
15 <140> CURRENT APPLICATION NUMBER: US 10/527,370
16 <141> CURRENT FILING DATE: 2005-03-10
18 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/11411
19 <151> PRIOR FILING DATE: 2003-09-08
21 <150> PRIOR APPLICATION NUMBER: JP 2002-264466
22 <151> PRIOR FILING DATE: 2002-09-10
24 <160> NUMBER OF SEQ ID NOS: 6
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 505
30 <212> TYPE: PRT
31 <213> ORGANISM: Cellulomonas sp. JCM2471
33 <400> SEQUENCE: 1
34 Met Ala Asp Tyr Val Leu Ala Ile Asp Gln Gly Thr Thr Ser Ser Arg
35 1      5      10      15
36 Ala Ile Val Phe Asn His Ser Gly Glu Ile Tyr Ser Thr Gly Gln Leu
37      20      25      30
38 Glu His Asp Gln Ile Phe Pro Arg Ala Gly Trp Val Glu His Asn Pro
39      35      40      45
40 Glu Gln Ile Trp Asn Asn Val Arg Glu Val Val Gly Leu Ala Leu Thr
41      50      55      60
42 Arg Gly Asn Leu Thr His Glu Asp Ile Ala Ala Val Gly Ile Thr Asn
43 65      70      75      80
44 Gln Arg Glu Thr Ala Val Val Trp Asp Lys Thr Thr Gly Lys Pro Val
45      85      90      95
46 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Gln Lys Ile Val Asp
47      100     105     110
48 Glu Leu Gly Gly Asp Glu Gly Ala Glu Lys Tyr Lys Ser Ile Val Gly
49      115     120     125
50 Leu Pro Leu Ala Thr Tyr Phe Ser Gly Pro Lys Ile Lys Trp Ile Leu
51      130     135     140
52 Asp Asn Val Glu Gly Ala Arg Glu Lys Ala Glu Lys Gly Asp Leu Leu
53 145     150     155     160
54 Phe Gly Asn Thr Asp Thr Trp Val Leu Trp Asn Met Thr Gly Gly Thr
55      165     170     175

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```

56 Glu Gly Gly Val His Val Thr Asp Val Thr Asn Ala Ser Arg Thr Met
57      180      185      190
58 Leu Met Asp Leu Asp Thr Leu Ser Trp Arg Glu Asp Ile Ala Ala Asp
59      195      200      205
60 Met Gly Ile Pro Leu Ser Met Leu Pro Asp Ile Arg Ser Ser Ser Glu
61      210      215      220
62 Val Tyr Gly His Gly Arg Pro Arg Gly Leu Val Pro Gly Val Pro Ile
63 225      230      235      240
64 Ala Gly Ile Leu Gly Asp Gln Gln Ala Ala Thr Phe Gly Gln Ala Cys
65      245      250      255
66 Phe Glu Val Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Asn Phe Leu
67      260      265      270
68 Leu Leu Asn Thr Gly Thr Glu Lys Val Met Ser Lys Asn Gly Leu Leu
69      275      280      285
70 Thr Thr Val Cys Tyr Lys Ile Gly Asp Ala Pro Ala Val Tyr Ala Leu
71      290      295      300
72 Glu Gly Ser Ile Ala Val Thr Gly Ser Leu Val Gln Trp Leu Arg Asp
73 305      310      315      320
74 Asn Leu Gly Met Phe Glu Asp Ala Pro Asp Val Glu Trp Leu Ala Gly
75      325      330      335
76 Lys Val Gln Asp Asn Gly Gly Ala Tyr Phe Val Pro Ala Phe Ser Gly
77      340      345      350
78 Leu Phe Ala Pro Tyr Trp Arg Pro Asp Ala Arg Gly Ala Leu Val Gly
79      355      360      365
80 Leu Thr Arg Tyr Val Asn Arg Asn His Ile Ala Arg Ala Ala Leu Glu
81      370      375      380
82 Ala Thr Ala Phe Gln Ser Arg Glu Val Val Asp Ala Met Asn Ala Asp
83 385      390      395      400
84 Ser Gly Val Asp Leu Thr Glu Leu Arg Val Asp Gly Gly Met Val Ala
85      405      410      415
86 Asn Glu Leu Leu Met Gln Phe Gln Ala Asp Gln Leu Gly Val Asp Val
87      420      425      430
88 Val Arg Pro Lys Val Ala Glu Thr Thr Ala Leu Gly Ala Ala Tyr Ala
89      435      440      445
90 Ala Gly Ile Ala Val Gly Phe Trp Lys Gly Glu Gln Asp Val Ile Asp
91      450      455      460
92 Asn Trp Ala Glu Asp Lys Arg Trp Ser Pro Ser Met Glu Ser Gly Glu
93 465      470      475      480
94 Arg Glu Arg Leu Tyr Arg Asn Trp Lys Lys Ala Val Thr Lys Thr Met
95      485      490      495
96 Glu Trp Val Asp Glu Asp Val Glu Gln
97      500      505
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 1515
101 <212> TYPE: DNA
102 <213> ORGANISM: Cellulomonas sp. JCM2471
104 <220> FEATURE:
105 <221> NAME/KEY: CDS
106 <222> LOCATION: (1)...(1515)

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108 <400> SEQUENCE: 2
109 atg gcc gac tac gtt ctc gcc atc gac cag ggg acc acg agc tcc cgg      48
110 Met Ala Asp Tyr Val Leu Ala Ile Asp Gln Gly Thr Thr Ser Ser Arg
111 1 5 10 15
113 gcc atc gtc ttc aac cac tcc ggg gag atc tac tcc acc ggg cag ctc      96
114 Ala Ile Val Phe Asn His Ser Gly Glu Ile Tyr Ser Thr Gly Gln Leu
115 20 25 30
117 gag cac gac cag atc ttc ccg cgc gcg ggc tgg gtc gag cac aac ccc      144
118 Glu His Asp Gln Ile Phe Pro Arg Ala Gly Trp Val Glu His Asn Pro
119 35 40 45
121 gag cag atc tgg aac aac gtg cgc gag gtc gtc ggt ctc gcc ctc acc      192
122 Glu Gln Ile Trp Asn Asn Val Arg Glu Val Val Gly Leu Ala Leu Thr
123 50 55 60
125 cga ggc aac ctc acg cac gag gac atc gcg gcc gtc ggc atc acg aac      240
126 Arg Gly Asn Leu Thr His Glu Asp Ile Ala Ala Val Gly Ile Thr Asn
127 65 70 75 80
129 cag cgc gag acg gcc gtc gtc tgg gac aag acc acg ggc aag ccc gtc      288
130 Gln Arg Glu Thr Ala Val Val Trp Asp Lys Thr Thr Gly Lys Pro Val
131 85 90 95
133 tac aac gcc atc gtc tgg cag gac acg cgc acc cag aag atc gtc gac      336
134 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Gln Lys Ile Val Asp
135 100 105 110
137 gag ctc ggc ggc gac gag ggc gcc gag aag tac aag tcg atc gtc ggc      384
138 Glu Leu Gly Gly Asp Glu Gly Ala Glu Lys Tyr Lys Ser Ile Val Gly
139 115 120 125
141 ctg ccg ctc gcc acc tac ttc tcc ggc ccg aag atc aag tgg atc ctc      432
142 Leu Pro Leu Ala Thr Tyr Phe Ser Gly Pro Lys Ile Lys Trp Ile Leu
143 130 135 140
145 gac aac gtc gag ggt gcg cgc gag aag gcc gag aag ggc gac ctg ctg      480
146 Asp Asn Val Glu Gly Ala Arg Glu Lys Ala Glu Lys Gly Asp Leu Leu
147 145 150 155 160
149 ttc ggc aac acc gac acg tgg gtg ctg tgg aac atg acg ggc ggc acc      528
150 Phe Gly Asn Thr Asp Thr Trp Val Leu Trp Asn Met Thr Gly Gly Thr
151 165 170 175
153 gag ggc ggc gtg cac gtc acc gac gtg acc aac gcg tcg cgc acg atg      576
154 Glu Gly Gly Val His Val Thr Asp Val Thr Asn Ala Ser Arg Thr Met
155 180 185 190
157 ctc atg gac ctc gac acg ctc tcc tgg cgc gag gac atc gcc gcc gac      624
158 Leu Met Asp Leu Asp Thr Leu Ser Trp Arg Glu Asp Ile Ala Ala Asp
159 195 200 205
161 atg ggc atc ccg ctg tcg atg ctc ccc gac atc cgg tcg tcg tcc gag      672
162 Met Gly Ile Pro Leu Ser Met Leu Pro Asp Ile Arg Ser Ser Ser Glu
163 210 215 220
165 gtc tac ggc cac ggg cgc ccg cgc ggc ctc gtc ccc ggc gtc ccg atc      720
166 Val Tyr Gly His Gly Arg Pro Arg Gly Leu Val Pro Gly Val Pro Ile
167 225 230 235 240
169 gcc ggc atc ctc ggc gac cag cag gca gcc acg ttc ggc cag gcg tgc      768
170 Ala Gly Ile Leu Gly Asp Gln Gln Ala Ala Thr Phe Gly Gln Ala Cys
171 245 250 255

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173 ttc gag gtc ggc cag gcc aag aac acc tac ggc acc ggc aac ttc ctg      816
174 Phe Glu Val Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Asn Phe Leu
175          260          265          270
177 ctg ctc aac acg ggc acg gag aag gtc atg agc aag aac ggc ctg ctc      864
178 Leu Leu Asn Thr Gly Thr Glu Lys Val Met Ser Lys Asn Gly Leu Leu
179          275          280          285
181 acg acg gtc tgc tac aag atc ggc gac gcg ccc gcg gtg tac gcg ctc      912
182 Thr Thr Val Cys Tyr Lys Ile Gly Asp Ala Pro Ala Val Tyr Ala Leu
183          290          295          300
185 gag ggc tcg atc gcc gtg acc ggc tcg ctc gtg cag tgg ctg cgc gac      960
186 Glu Gly Ser Ile Ala Val Thr Gly Ser Leu Val Gln Trp Leu Arg Asp
187 305          310          315          320
189 aac ctg ggc atg ttc gag gac gcg ccc gac gtc gag tgg ctc gcg ggc      1008
190 Asn Leu Gly Met Phe Glu Asp Ala Pro Asp Val Glu Trp Leu Ala Gly
191          325          330          335
193 aag gtc cag gac aac ggc ggc gcc tac ttc gtg ccg gcg ttc tcc ggc      1056
194 Lys Val Gln Asp Asn Gly Gly Ala Tyr Phe Val Pro Ala Phe Ser Gly
195          340          345          350
197 ctg ttc ggc ccc tac tgg cgg ccc gac gcg ggc ggc ctc gtc ggc      1104
198 Leu Phe Ala Pro Tyr Trp Arg Pro Asp Ala Arg Gly Ala Leu Val Gly
199          355          360          365
201 ctc acg cgg tac gtc aac cgc aac cac atc gcg cgc gcc gcg ctc gag      1152
202 Leu Thr Arg Tyr Val Asn Arg Asn His Ile Ala Arg Ala Ala Leu Glu
203          370          375          380
205 gcg acg gcg ttc cag agc cgc gag gtc gtc gac gcg atg aac gcc gac      1200
206 Ala Thr Ala Phe Gln Ser Arg Glu Val Val Asp Ala Met Asn Ala Asp
207 385          390          395          400
209 tcg ggc gtc gac ctc acc gag ctg cgc gtc gac ggc ggc atg gtc gcc      1248
210 Ser Gly Val Asp Leu Thr Glu Leu Arg Val Asp Gly Gly Met Val Ala
211          405          410          415
213 aac gag ctc ctc atg cag ttc cag gcc gac cag ctc ggc gtc gac gtc      1296
214 Asn Glu Leu Leu Met Gln Phe Gln Ala Asp Gln Leu Gly Val Asp Val
215          420          425          430
217 gtg cgg ccc aag gtc gcc gag acg acg gcg ctc ggt gcc gcg tac gcc      1344
218 Val Arg Pro Lys Val Ala Glu Thr Thr Ala Leu Gly Ala Ala Tyr Ala
219          435          440          445
221 gcg ggc atc gcc gtc ggc ttc tgg aag ggc gag cag gac gtc atc gac      1392
222 Ala Gly Ile Ala Val Gly Phe Trp Lys Gly Glu Gln Asp Val Ile Asp
223          450          455          460
225 aac tgg gcc gag gac aag cgc tgg agc ccg tcg atg gag tcc ggc gag      1440
226 Asn Trp Ala Glu Asp Lys Arg Trp Ser Pro Ser Met Glu Ser Gly Glu
227 465          470          475          480
229 cgc gag cgg ctg tac cgc aac tgg aag aag gcc gtg acg aag acg atg      1488
230 Arg Glu Arg Leu Tyr Arg Asn Trp Lys Lys Ala Val Thr Lys Thr Met
231          485          490          495
233 gag tgg gtc gac gag gac gtg gag cag      1515
234 Glu Trp Val Asp Glu Asp Val Glu Gln
235          500          505
238 <210> SEQ ID NO: 3

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239 <211> LENGTH: 23  
240 <212> TYPE: DNA  
241 <213> ORGANISM: Artificial Sequence  
243 <220> FEATURE:  
244 <223> OTHER INFORMATION: primer  
246 <400> SEQUENCE: 3  
247 tacgtsctsg csatcgacca ggg 23  
249 <210> SEQ ID NO: 4  
250 <211> LENGTH: 27  
251 <212> TYPE: DNA  
252 <213> ORGANISM: Artificial Sequence  
254 <220> FEATURE:  
255 <223> OTHER INFORMATION: primer  
257 <400> SEQUENCE: 4  
258 ttcttggtgsa tgccstgscsacgaag 27  
260 <210> SEQ ID NO: 5  
261 <211> LENGTH: 23  
262 <212> TYPE: DNA  
263 <213> ORGANISM: Artificial Sequence  
265 <220> FEATURE:  
266 <223> OTHER INFORMATION: primer  
268 <400> SEQUENCE: 5  
269 atatcggtgc gctcgaccag ggc 23  
271 <210> SEQ ID NO: 6  
272 <211> LENGTH: 23  
273 <212> TYPE: DNA  
274 <213> ORGANISM: Artificial Sequence  
276 <220> FEATURE:  
277 <223> OTHER INFORMATION: primer  
279 <400> SEQUENCE: 6  
280 tcgtgttctt cccacgccat cgc 23

**VERIFICATION SUMMARY**

DATE: 03/03/2006

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Input Set : A:\18965-002US1.TXT

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